

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/822,235 A
Source: IFW/6
Date Processed by STIC: 05/17/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>10/822,235A</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 ____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 ____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text .	
5 ____ Variable Length	Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 ____ Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 ____ Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional , please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 ____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents.	
10 ____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)	
11 ____ Use of <220>	Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules	
12 ____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ____ Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFW16

RAW SEQUENCE LISTING

DATE: 05/17/2006

PATENT APPLICATION: US/10/822,235A

TIME: 10:44:38

Input Set : A:\SEQLIST - text.txt

Output Set: N:\CRF4\05172006\J822235A.raw

4 <110> APPLICANT: Susan Gould-Fogerite
 5 Raphael Mannino
 6 Patrick Ahl
 7 Gaofeng Shang
 8 Zi Wei Chen
 9 Sara Krause
 11 <120> TITLE OF INVENTION: COCHLEATE COMPOSITIONS DIRECTED AGAINST
 12 EXPRESSION OF PROTEINS
 16 <130> FILE REFERENCE: BSZ-049
 18 <140> CURRENT APPLICATION NUMBER: 10/822,235A
 19 <141> CURRENT FILING DATE: 2004-04-09
 21 <160> NUMBER OF SEQ ID NOS: 16
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Does Not Comply
 Corrected Diskette Needed
 (pgs 1,2)

ERRORED SEQUENCES

165 <210> SEQ ID NO: 13
 166 <211> LENGTH: 5
 E--> 167 <212> TYPE: Protein
 168 <213> ORGANISM: Peptide
 170 <220> FEATURE:
 171 <223> OTHER INFORMATION: Aspergillus fumigatus
 173 <400> SEQUENCE: 13
 174 Thr Gly Glu Ser Leu
 175 1 5
 177 <210> SEQ ID NO: 14
 178 <211> LENGTH: 6
 E--> 179 <212> TYPE: Protein
 180 <213> ORGANISM: Peptide
 182 <220> FEATURE:
 183 <223> OTHER INFORMATION: Aspergillus fumigatus
 187 <400> SEQUENCE: 14
 188 Cys Ser Asp Lys Thr Gly
 189 1 5
 191 <210> SEQ ID NO: 15
 192 <211> LENGTH: 5
 E--> 193 <212> TYPE: Protein
 194 <213> ORGANISM: Peptide
 196 <220> FEATURE:
 197 <223> OTHER INFORMATION: Aspergillus fumigatus
 199 <400> SEQUENCE: 15
 200 Met Xaa Thr Gly Asp

L2127 Represents
 DNA/RNA/PRT

Invalid Response.
 L2137 Responses can
 be either Artificial,
 Unknown or Genus
 Species. Pls see glen.
 10 in error summary
 sheet.

Same Error

Same Error

RAW SEQUENCE LISTING

DATE: 05/17/2006

PATENT APPLICATION: US/10/822,235A

TIME: 10:44:38

Input Set : A:\SEQLIST - text.txt

Output Set: N:\CRF4\05172006\J822235A.raw

201 1 5
203 <210> SEQ ID NO: 16
204 <211> LENGTH: 8
E--> 205 <212> TYPE: Protein
206 <213> ORGANISM: Peptide
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Aspergillus fumigatus
211 <400> SEQUENCE: 16
212 Gly Asp Gly Xaa Asn Asp Xaa Pro
213 1 5
224 Attorney Docket Number: BSZ-049
226 -1-

*Same Error**Same Error**Pls delete.*3
f

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/822,235A

DATE: 05/17/2006

TIME: 10:44:39

Input Set : A:\SEQLIST - text.txt

Output Set: N:\CRF4\05172006\J822235A.raw

L:167 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:13
L:179 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:14
L:193 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:15
L:205 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:16